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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Fri Sep 14 16:42:52 EDT 2007

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\*\*\*\*\*

Reviewer Comments:

<213> Aphis gossyii

In the above "<213>" response, do you mean "Aphis gossypii?"

<400> 9

cgacuggagc acgaggacac ugacauggac ugaaggagua gaaa

44

19

60294-PCT

11

Please remove the above numbers and text, which appear at the end of the submitted file.

\*\*\*\*\*

Application No: 10538989 Version No: 1.0

Input Set:

Output Set:

Started: 2007-09-04 14:59:17.201  
 Finished: 2007-09-04 14:59:18.420  
 Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 219 ms  
 Total Warnings: 12  
 Total Errors: 6  
 No. of SeqIDs Defined: 9  
 Actual SeqID Count: 9

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (9)
W 112	Upper case found in data; Found at position(50) SEQID(9)
W 112	Upper case found in data; Found at position(51) SEQID(9)
W 112	Upper case found in data; Found at position(52) SEQID(9)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 53 SEQID(9)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (9)
E 253	The number of bases differs from <211> Input: 44 Calculated:53



# SEQUENCE LISTING

<110> FMC Corporation  
Wu, Shilan  
Allenza, Paul  
Halling, Blaik

<120> Aphis gossypii Polo-like Kinases

<130> 60294

<140> 10538989

<141> 2007-09-04

<160> 9

<170> PatentIn version 3.1

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<211> 2240

<212> DNA

<213> Aphis gossypii

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<212> PRT  
<213> Aphis gossypii

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Lys Gly Gly Phe Ala Lys Cys Tyr Glu Ile Val Asp Leu Lys Thr Lys  
35 40 45

Glu Ile Phe Ala Gly Lys Ile Val Ser Lys Lys Tyr Leu Leu Lys His  
50 55 60

Asn Gln Lys Asp Lys Met Thr Gln Glu Ile His Ile His Lys Met Leu  
65 70 75 80

Lys His Thr Asn Ile Val Thr Phe His Ser Phe Phe Glu Asp Asn Asp  
85 90 95

Phe Val Tyr Ile Val Leu Glu Leu Cys Arg Lys Arg Ser Met Met Glu  
100 105 110

Leu His Lys Arg Arg Lys Thr Leu Thr Glu Pro Glu Thr Arg Tyr Tyr  
115 120 125

Val Phe Gln Ile Leu Glu Gly Thr Leu Tyr Leu His Asn Gln Gly Ile  
130 135 140

Ile His Arg Asp Leu Lys Leu Gly Asn Leu Phe Leu Asn Asp Glu Met  
145 150 155 160

Glu Val Lys Ile Gly Asp Leu Gly Leu Ala Ala Arg Ile Glu Tyr Asp  
165 170 175

Gly Gln Arg Lys Lys Thr Leu Cys Gly Thr Pro Asn Tyr Ile Ala Pro  
180 185 190

Glu Ile Leu Ser Lys Thr Gly His Ser Phe Glu Val Asp Val Trp Ser  
195 200 205

Ile Gly Cys Ile Met Tyr Thr Leu Leu Val Gly Lys Pro Pro Phe Glu  
210 215 220

Thr Asn Ser Leu Lys Glu Thr Tyr Ala Arg Ile Ala Arg Cys Asp Tyr  
225 230 235 240

Ser Leu Pro Pro His Leu Asn Lys Asn Ala Ser Ser Leu Ile Asn Lys  
245 250 255

Met	Leu	Gln	Tyr	Asp	Pro	Lys	Lys	Arg	Pro	Cys	Val	Ser	Asp	Ile	Met				
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Lys	Ala	Asp	Phe	Phe	Thr	Thr	Gly	Tyr	Met	Pro	Lys	Lys	Leu	Pro	Pro				
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Ser	Cys	Leu	Thr	Met	Ala	Pro	Arg	Phe	Asp	Ser	Ile	Asn	Tyr	Arg	Glu				
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Ser	Ile	Ser	Asn	Arg	Arg	Pro	Leu	Asn	Glu	Leu	Asn	Ser	Pro	Lys	Ala				
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Ala	Ile	Ile	Lys	Val	Ala	Ser	Lys	Pro	Gln	Asp	Pro	Val	Asn	Lys	Leu				
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Pro	Met	Phe	Asn	Ile	Pro	Asn	Lys	Pro	Thr	Thr	Gly	Asn	Gly	Val	Ser				
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Ser	Asn	Asp	Cys	Lys	Glu	Tyr	Met	Met	Ser	Leu	Glu	Arg	Glu	Leu	Gly				
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Asn	Leu	Leu	Lys	Cys	Lys	Pro	Thr	Met	Lys	Gly	Met	Lys	Asn	Met	Glu				
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Glu	Asn	Thr	Asp	Pro	Ala	Ala	Gln	Pro	Leu	Ile	Trp	Val	Ser	Lys	Trp				
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Val	Asp	Tyr	Ser	Asp	Lys	Tyr	Gly	Phe	Gly	Tyr	Glu	Leu	Ser	Asp	Asp				
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Cys	Val	Gly	Val	Met	Phe	Asn	Asp	Phe	Thr	Arg	Ile	Val	Leu	Leu	Ala				
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Asn	Leu	Lys	Asp	Val	His	Tyr	Ile	Glu	Arg	Asn	Gly	Ser	Glu	Gln	Tyr				
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His	Thr	Thr	Glu	His	Thr	Pro	Pro	Ser	Leu	Glu	Lys	Lys	Met	Lys	Leu				
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Leu	Met	Tyr	Phe	Arg	Arg	Tyr	Met	Asn	Asp	His	Leu	Ile	Lys	Ala	Gly				
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Ala Asp Ile Leu Ala Lys Asp Ala Asp Gln Leu Ser Arg Thr Pro Tyr  
485 490 495

Met Tyr Gln Trp Tyr Arg Ser Thr Ser Ser Val Ile Met Gln Leu Thr  
500 505 510

Asn Gly Thr Leu Gln Ile Asn Phe Thr Asp His Thr Lys Val Ile Leu  
515 520 525

Cys Pro Leu Met Asn Ala Val Thr Phe Ile Glu Asn Asn Val Phe Arg  
530 535 540

Thr Tyr Arg Phe Asn Thr Ile Ala Glu His Gly Cys Ser Pro Glu Leu  
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Gly Lys Cys Leu Glu Tyr Ala His Lys Lys Ile Gly Ser Ile Leu Lys  
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Asp Ser Pro Val  
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ctcaatagcc ccaaagctgc catcattaaa gttgcttcta aacctcaaga tccggttaat 180  
aaattgccaa tgtttaatat tccaaataaa ccaactactg gaaatgggtg ttcattccaat 240  
gactgtaaag aatacatgat gtcccttgaa agagaattgg gaaatttatt gaaatgtaaa 300  
ccaaccatga aaggaatgaa aaacatggag gaaaacactg acccagctgc tcaacctctc 360  
atttggggtta gtaaattggg ggactattcc gataaatatg gatttggata tgaattatct 420  
gatgattgtg ttggtgttat gttcaatgat ttaccagaa tagtactttt agccaatcta 480  
aaagatgtcc attacataga aagaaatggg tcagaacaat accatacaac tgaacatact 540  
ccaccgtcgt tagagaaaaa aatgaagtta ttgatgtact tcagacgtta catgaatgat 600  
catcttatta aagctgggtgc tgatatatta gctaaagatg cagaccaatt gagtcgtaca 660  
ccatacatgt accaatggta taggtctact tcatcagttt ttatgcaact tactaacggc 720



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ggctgtagcc ctgaattagg aaaatgcttg gaatatgctc acaagaaaat tggatctata      900
ttaaagata gccagttta atttacttga aaattgacga gtatatntag tttatagtta      960
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              20              25              30

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Ser Asn Arg Arg Pro Leu Asn Glu Leu Asn Ser Pro Lys Ala Ala Ile
              35              40              45

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Ile Lys Val Ala Ser Lys Pro Gln Asp Pro Val Asn Lys Leu Pro Met
50              55              60

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Phe Asn Ile Pro Asn Lys Pro Thr Thr Gly Asn Gly Val Ser Ser Asn
65              70              75              80

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Asp Cys Lys Glu Tyr Met Met Ser Leu Glu Arg Glu Leu Gly Asn Leu
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Leu Lys Cys Lys Pro Thr Met Lys Gly Met Lys Asn Met Glu Glu Asn
100              105              110

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Thr Asp Pro Ala Ala Gln Pro Leu Ile Trp Val Ser Lys Trp Val Asp
115              120              125

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Tyr Ser Asp Lys Tyr Gly Phe Gly Tyr Glu Leu Ser Asp Asp Cys Val  
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Gly Val Met Phe Asn Asp Phe Thr Arg Ile Val Leu Leu Ala Asn Leu  
145 150 155 160

Lys Asp Val His Tyr Ile Glu Arg Asn Gly Ser Glu Gln Tyr His Thr  
165 170 175

Thr Glu His Thr Pro Pro Ser Leu Glu Lys Lys Met Lys Leu Leu Met  
180 185 190

Tyr Phe Arg Arg Tyr Met Asn Asp His Leu Ile Lys Ala Gly Ala Asp  
195 200 205

Ile Leu Ala Lys Asp Ala Asp Gln Leu Ser Arg Thr Pro Tyr Met Tyr  
210 215 220

Gln Trp Tyr Arg Ser Thr Ser Ser Val Ile Met Gln Leu Thr Asn Gly  
225 230 235 240

Thr Leu Gln Ile Asn Phe Thr Asp His Thr Lys Val Ile Leu Cys Pro  
245 250 255

Leu Met Asn Ala Val Thr Phe Ile Glu Asn Asn Val Phe Arg Thr Tyr  
260 265 270

Arg Phe Asn Thr Ile Ala Glu His Gly Cys Ser Pro Glu Leu Gly Lys  
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Cys Leu Glu Tyr Ala His Lys Lys Ile Gly Ser Ile Leu Lys Asp Ser  
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Pro Val  
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